FIG. 1A

```
1     AAGCTTTCTTGGCCCCTAACAGCAACCACATTATACTCTTACTGGCTATTCCTTGGCCTT   60
61    CAATACCCAGCCCAGGGGACCCCTCTTCCAGGGAGCCCCGCTTGTACTCCTGAGATGTCA   120
121   TGTCCTTCTTGCAGAGCTCTTCCTCACGGCATCGGGACGGCGGTTCACCCTTTTGCCTCT   180
181   CCGGATAAACTGTAAGCTACTTGAGAGCAGAGAACATCCATTGTTCGCTGTGGCATCCGT   240
241   GGTACCTAGCACGGCATCTGACATATTATCAGATCTTCCACAAAGGCCAGTTTACGGTTG   300
301   AATGCCCGTTGAATTCAGGCTCCCAGTGGGAGAGCGAGGAAGTAATAAAGCCGGTGATAA   360
361   ATGCCGCCGTGGAGACACCAGCGGGCTGCCGTGAGACTAATGGAGAGGACAGTAACGTTA   420
421   TCTCTAATGCGAGGGTGGTTATAGAGTACATTTCATAACACCTTTAAAGCTCTTTCACAC   480
481   GCATTATCCAATTTGATCCTCATAAAAGCCTGGAGATGTGTATATTGTGGTGGATGGAGG   540
541   GGGAGTCTTTAGCAGTTATGGGATATGCCTGAAGTCGTGCAGCTAGTAAATGGCTGGATT   600
601   CAAACCAGACCTCAAAAGCCTGCCTGTTTGCTCATGCCCCCTGCCCCGACTGCCCACTCT   660
661   GTGGCCCACAGCACAACTCACCGTCGCTTTCTTGATCCGTTTTCTTGATCCGGCTGTGCT   720
721   CTCCCCAAGGAATGCTTTTCATTAACATATGTCTAGGTAATGAATTATCTTGACTCTGAG   780
781   GAGGCCATAGCACATGCCGTAACGCGACAGCTCCTTTGATCTGCATCTGAGGCTGTGGCT   840
841   GGTAACGGGCGTGGGGAGGGGGCGTTCGCTGAGACCCCAGGGACACGCCATGTGTGGTTC   900
901   CCTCTGTTTCCAGGCCCCAGAAGCACATCCCGGAAAGGAAAATGCGCTGTGGACCCCTGT   960
                                                      M  R  C  G  P  L  C
961   GCCGATTCCTGCTGGCTTTGGCCTATCTGTCCTACGTTGAAGCCGTGCCCATCTGGAGAG   1020
       R  F  L  L  A  L  A  Y  L  S  Y  V  E  A  V  P  I  W  R  V
1021  TCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACCAGGATCAGTGACATTTCAC   1080
       Q  D  D  T  K  T  L  I  K  T  I  V  T  R  I  S  D  I  S  H
1081  ACATGGTAGGGAAGGCCTGGGAGACAAGGTCGAACCTGTGGCCAGCCCSGGGGGAGGAGG   1140
       M
1141  GGTACCGGACCTCAGAGGTTGGCGGAGGTGGGAAGGGTCGGCGGTGGCCTTGACGCCTCC   1200
1201  CCCACCCCCCCCAACCAGCTGCCTTTGCTCCTCCGCTTCCCTCACCGCACCCCCCCACGT   1260
1261  CCTTATCCTCCTTCTTCCCAGACTGGAATCCTGATGCCCAGGACTAGAGGAAGCCCTAAA   1320
1321  GGTCCTGTGTGCCTTTGCCAGGTGCGCAGACCCCCCAGCATCATCCCCTCTGGCCTCCAT   1380
1381  CACGTCTCCGGAATGTTCTAATCTGTAGGAATTCTTCCTGGTGACAGCTGAACTCTGACC   1440
1441  CTGCGGACGCCCCTTACTGCTAGTCCTGCCCATTGAGCCTTTTTTCCTATACAACCCTCT   1500
1501  ACATGTTTGCAAACTTCTCTCAATGTCCCCAGGGTGTTTTCTCTGGGGTCCGCAGGCCGA   1560
1561  GACCTTCAGCCTCTTCTCAGCTGAGGTCCGTCTTTAGAATTCAGAAGACGAGGTGTGACT   1620
1621  CCTCACCCTGCTGTTCCCTCTCTGTAAAATCTCAAGCACGTTAAGTCCCTCCGTGTCTGA   1680
1681  AACCTTAGTTTCCCTCATCCAGATAATGGGACTGTTACTGGGAAGATGTTACCGGAATCC   1740
1741  AGGGTCTTGCCTCATGGAGCTCAAGAATGAACTTGGCGAACGCACAGGGAGCCGAGCAAG   1800
```

FIG. 1B

```
1801  CAGAAGTCTTTATTACAGGAAGGCAGACAGCTCCCAGCACAGACACGGGGAGGGAAGAGT  1860
1861  CCCCCCGCCCATTGTTCTACGGAGGTTTTTATCACTTAAAGACGGGAGTACCAATGTGGG  1920
1921  GTCCAGATATCCGTTCTTCTTCCCATTGCCCAGTTTACCTATATGGCGCCTTGTCCAGGA  1980
1981  GGGACTCTGTAGAGTTAGGGGTGCTCCGTAAGTTTTATGGTGCGTCTGCTCTTCTCTGCC  2040
2041  CTAGACTTAGAGTCGCCACTCTTTCCATTCTTCTGCTCACAGTCAAATGCATAGGTCAGG  2100
2101  GGTTAATTCCCACCTTCACAGAAATCAAATGTCCTTTCAATAGTTAATCTTCCAATAAGC  2160
2161  AAGGCCTGCTTGTCTTGATTAGTTTTTACAAATCTTAAACCATGGCCATTAATCAGGGAA  2220
2221  GAGATCGAAGCCCATGTTCCCACACTAACTGCCTGAATTATTAGTCTGCCTCAGGACTAT  2280
2281  CTTAATAGTCTTCGCAAGGTTGTTTTGAGATTAAATTAGATAGGAGTTCCTGTCGAGGCG  2340
2341  CGACGGAAACAGATCCGACTCAGAACCATGAGACAGGTTCGATCCCTGGCTTTGTCAGTG  2400
2401  GGTTAGGATCTGGTGCTGCTGTGAGCTGTGGTGTAGGTCGCAGAGGTGGCTCGGATCCCG  2460
2461  CGTTGCTGTGGCTGTGGTGTAGGCCGGTGCAGACAGCTCCGATTAGACCCCTAGCCTGGG  2520
2521  AACCTCCATGTGCCGCGGGTACCGCTAAAAAAAGACAAAAGATGGAAAAAAAAAAGGTTA  2580
2581  CATTAGATAAAGCAAGTGACTCCTCCACCACCACACATATCCCTGCAGAACCAGGACAGA  2640
2641  GCATGCCTTCTTGAAAAGTTTTCGGTTGTGGCTTTGATAGCACCCAGCCTTAAAAGCCAG  2700
2701  CTTTTCAATCTGCCCAGAGCAGTCTGGAGACTTCCGCATCTCCTGGCCACTCTGAGTTTC  2760
2761  TAACAGTGGCCTTGGCGAGCCTGGGAGCAGTCCGGTGGCCAGAAGCAGGGACAGCTGAGA  2820
2821  ACCAGATAGAGTCTTGGCACTTTCAAGAGAAAACCCTAAGTCTCCTTCTTCCAGCCATGC  2880
2881  AACAGCTGCGCATGACAGATCCAGCGTGTCCCAGCCTGTGTGGTGCAGGGAGTGAYGCTG  2940
2941  CGNNYAGGGYGYGGGGGAGCTGAGGAGCGAGGCGGGGCATCGNGGGGCTGCAGCCTCCAT  3000
3001  CCCTAAGTGGGGAGACTTCATGAAGAGCCTGACCAGNAGGGAGGGGCATGTGTGGAGGAC  3060
3061  CTCAGGGCCTGGGGAAGGCTAGACCCAACTATGTGAGAAACAGACAGTCGTGGCTGGTTC  3120
3121  TACAGAAGAGGCATCTGGAGGCCATTCGAATGCCCAAAGCTGTCTGGGTGAGGCAGGGCT  3180
3181  TGCTAGGCAGAAGACAGAAGGCCGTGAGACCAGCTTGGAGGCTTGGCAGCCACGCCAGCC  3240
3241  CAAGGAGTTCGGGCCTAGATAGGATTGTGTGGAAGGGGAAGAGGCAGCCGGAGGTGGGGG  3300
3301  GTGGGGGTGGACCCGTCTCCACGCCTGCAGGAAGGCCAGGGGCTGCAGAGCCAACATCTC  3360
3361  TCTCGCTGAGCGTCTCGCTCTCCCCTTCCTCCTGCACAGCAGTCTGTCTCCTCCAAACAG  3420
                                                    Q  S  V  S  S  K  Q
3421  AGGGTCACCGGTTTGGACTTCATCCCTGGGCTCCATCCTGTCCTGAGTTTGTCCAAGATG  3480
      R  V  T  G  L  D  F  I  P  G  L  H  P  V  L  S  L  S  K  M
3481  GACCAGACCCTGGCGATCTACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATC  3540
      D  Q  T  L  A  I  Y  Q  Q  I  L  T  S  L  P  S  R  N  V  I
3541  CAAATATCGAATGACCTGGAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCCTCCAAG  3600
      Q  I  S  N  D  L  E  N  L  R  D  L  L  H  L  L  A  S  S  K
3601  AGCTGCCCCTTGCCCAGCAGGGcCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCCTGGAA  3660
      S  C  P  L  P  S  R  A  L  E  T  L  E  S  L  G  G  V  L  E
```

FIG. 1C

3661 GCCTCCCTCTACTCCACGGAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGAC 3720
A S L Y S T E V V A L S R L Q G A L Q D

3721 ATGCTGCGGCAGCTGGACCTCAGCCCTGGCTGCTGAAGCCTTGAAGGCCTCTCTCCCCAC 3780
M L R Q L D L S P G C *

3781 AGTCGGGGGAAGAAACCTGAGCTTCCAGGAGTCTGCTGGAGAAGAGAGCCTGTGCGGACC 3840

3841 TCCTCTCTGCAGGTCTGCGGACCATTTCTCTCTCGCTCCGCTAAGCTGCTCTTCCAAAGG 3900

3901 CAGAAAACTCCAAGGCACGACACCAAAGACAGAAAGGCCTGGTTCCGCGCCCACCGGAAA 3960

3961 GGGGGCGCCGTCCAGCCAACGGTGGACTAGATTTCGGATTTTCCACCAACGTCTTCCTTC 4020

4021 CTGTTCCATCTCCAGCTCACCGCGTGCTTCAGCGTGACCGGGGGGATTTCAGAGCCTTTC 4080

4081 GACCATCAAGCAGGGTTCCATCTGAGAATTCCGGGGAGCACGGTGAAGGCTACAGGCACA 4140

4141 CACAGCTGGATGCTCCCACGCAACACAAGTTGGAAGCATTTCTTTATTTATTATGCGGTG 4200

4201 TATTCTGGTTGGATTTGAAGCAAAACACCAGCCTTTCCAGGCTCTCTGGGGTCAGCCGGG 4260

4261 GCTAGGGGGAGGCTCCCGAGGTGCTGTTTCCAGTACCATCCATGGGCCTGCTGAGGCCAA 4320

4321 CCCATTTTGAGTGACTTGAGGGCTCTCAAGGTCGTTCTCTAGAGACTGGCTTTGTTTCTA 4380

4381 CTGTGACTGACTTTAAAACTGCAGCGTGTGCACTGGCATCGCCTGCGCGGATCTCGAAGG 4440

4441 GCCAGGTTCTCTTAGAAAGAAGAAGATGAACTTTGTCAGGGGTGTGTACGCGGAGACAGG 4500

4501 AAGTGTGTTGGTGGGCGGGGCATGGATCCAGAATGTGTATTTCTTGTGTGATGGACATTT 4560

4561 GTGTGAGGGGCTCTCTGGACAGGGTGAGGTCATTGTCTCATCTTCGTGGTTTTCATGAGA 4620

4621 GAAGGAGATGATTCCTTCACGGGGGTCGTGGGGTTTTGCCAGCCGCCCGTGCAGGAGTGG 4680

4681 GGAAGGGGCTGAAGCCGAAGACCGTTGGGGGCCGTGGTGAGCTCTGCCTTCTCCAGCTGC 4740

4741 TAGAGGCTGGTCTTTCTCATCAGGGAGTGAGGGTCTCGCGTTGGAGACAGTGATCCCCAG 4800

4801 GGCGGGATCCTTGCCGTGGCCCTCTGAATGGTCTGGGTGATCCCACACTGATGTCATAAC 4860

4861 AGGGAAGTGCCCTGGTTTGGGATTTGTATGCTCACCCAAAGCAAGGGCCTGCTTCCCATC 4920

4921 CATTTTGGGAAGGATTTTTTCTCCAGGGGGAGGGTGAAAGCTCTGGGAGGTCTGTGGGCT 4980

4981 TACGAGATGGTCCAAGTCCTGGGTCAGTGAGTCCCGGGACTCGTGACCGCCTCGAGGAGC 5040

5041 CCCCTTCTCCCTACAGGTCATGTTCAATAGGTCAAACAAGGAGGCATGGGTTTCCACCAT 5100

5101 CCTGCCGCTGTGATGCAGCCATCGCACTACAGGAGGTAGATCTGTCCAAGGAAATTTGAA 5160

5161 TCTCAAGCAATCACTTTCAAGACTGAGCATCTATTGTGCTCAGCCCCAACTGGTGCTATG 5220

5221 GGCTCAGAGAAGCTCATCAAATAAATATTAAAATCCAGTCCTGCCTTCAGGACCTTGCAT 5280

5281 TCCAGATGATAACACCTCCCCCACACCCCGTCTGCAGAGGCTGTCATTTCACCATGGCAA 5340

5341 CCGAGCAGCTGAAACACAGTGCGGTCCTCAGCAGGTGGAAAGGCTGAGCTGAGGAGGGCA 5400

5401 GTGCCCGGGCCCACAGGCTAACCCTGCTTGCACTTGGTAGCATTTTTACTGTTCGGGGCG 5460

5461 CATCAGCATCTATTACTGAGAAGCCGCATCCCTTTGAAGCAGGATAGCTGAGACTATAAA 5520

5521 AATAAGAAAATACCAGAGTTCCCTTGTGGCACAGAGGGCTAAGGATCCAGTGTTGTTGCT 5580

5581 GCAGCAGCTTGGGTCACGGCTGTGGCAAGGGTTCGATCCCTGGCCTGGGAACTTTCACAT 5640

FIG. 1D

```
5641  GTTGCAGGCAAGGCCAAAAAAAAAATAAATAAATAAAAATAAACAAAAAAAAAACAAGACCA  5700
5701  TAACAGCAGACTGGTGGCAAACCAGGACTAGAACCTGGGTCCTCTGACCCCTAGAGTCAG  5760
5761  TGTCCCCTGAGCCAGCTAGTGTTCTCTGGGGACGGGAACAGGGTTGGGCAGGGAGTTCAG  5820
5821  GAAGTGTTTGCTGGAAGAGCGGAGTTTCCAGGCTGATTTTGCAGGAGGTGAGGGAAGTGG  5880
5881  ATTGCCTGGAGGGAGGAGGCTGTTTTGTTTGAAGCTT                          5917
```

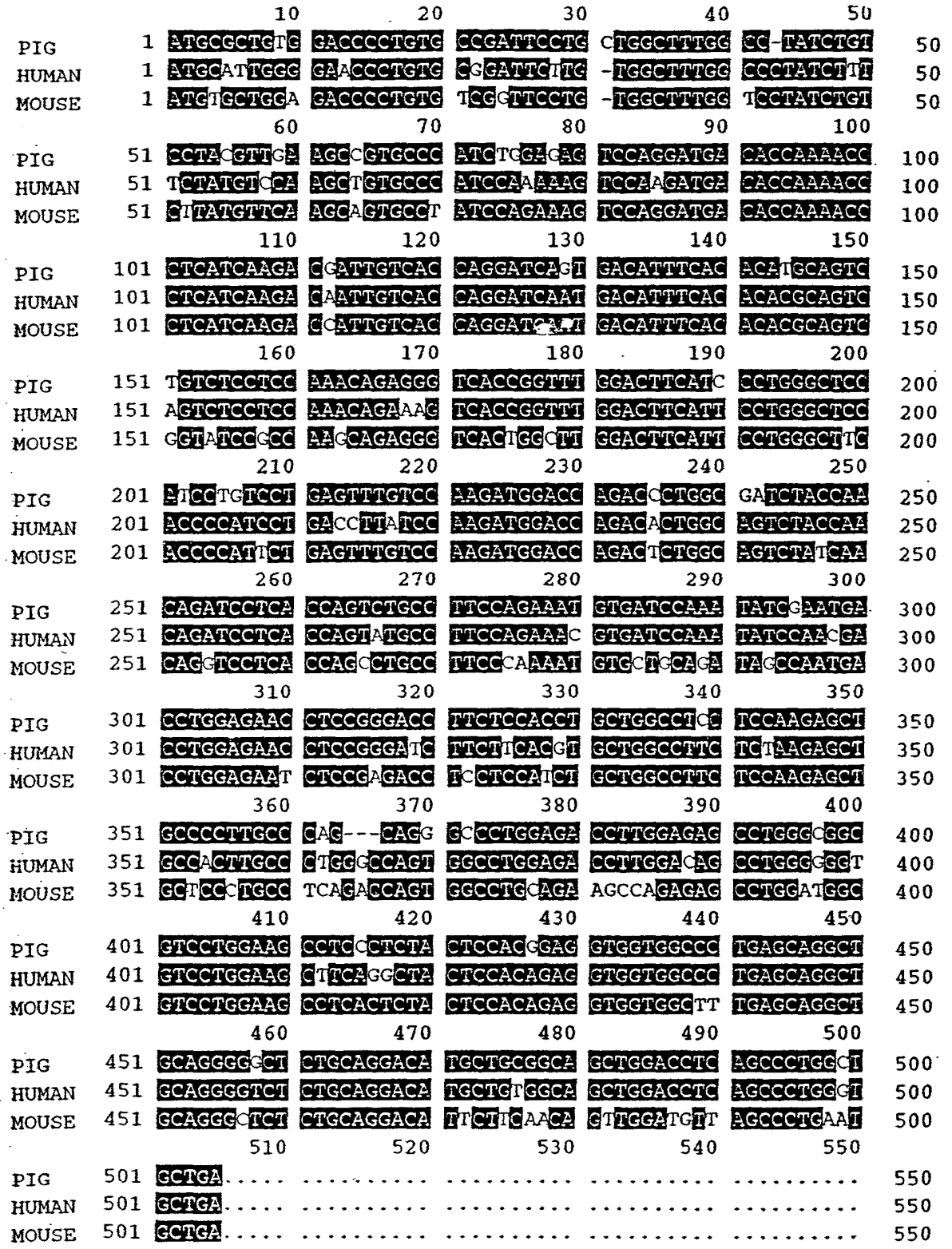
FIG. 2

```
Size     501 , Select        1
   1 ATGCGCTGTGGACCCCTGTGCCGATTCCTGCTGGCTTTGGCCTATCTGTCCTACGTTGAA     60

   1   M  R  C  G  P  L  C  R  F  L  L  A  L  A  Y  L  S  Y  V  E     20

  61 GCCGTGCCCATCTGGAGAGTCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACC    120

  21   A  V  P  I  W  R  V  Q  D  D  T  K  T  L  I  K  T  I  V  T     40

 121 AGGATCAGTGACATTTCACACATGCAGTCTGTCTCCTCCAAACAGAGGGTCACCGGTTTG    180

  41   R  I  S  D  I  S  H  M  Q  S  V  S  S  K  Q  R  V  T  G  L     60

 181 GACTTCATCCCTGGGCTCCATCCTGTCCTGAGTTTGTCCAAGATGGACCAGACCCTGGCG    240

  61   D  F  I  P  G  L  H  P  V  L  S  L  S  K  M  D  Q  T  L  A     80

 241 ATCTACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATCCAAATATCGAATGAC    300

  81   I  Y  Q  Q  I  L  T  S  L  P  S  R  N  V  I  Q  I  S  N  D    100

 301 CTGGAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCCTCCAAGAGCTGCCCCTTGCCC    360

 101   L  E  N  L  R  D  L  L  H  L  L  A  S  S  K  S  C  P  L  P    120

 361 AGCAGGGCCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCCTGGAAGCCTCCCTCTACTCC    420

 121   S  R  A  L  E  T  L  E  S  L  G  G  V  L  E  A  S  L  Y  S    140

 421 ACGGAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGACATGCTGCGGCAGCTG    480

 141   T  E  V  V  A  L  S  R  L  Q  G  A  L  Q  D  M  L  R  Q  L   160

 481 GACCTCAGCCCTGGCTGCTGA                                          501

 161   D  L  S  P  G  C  *                                           167
```

FIG. 3

```
  1 GTGCCCATCTGGAGAGTCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACCAGG   60
  1   V  P  I  W  R  V  Q  D  D  T  K  T  L  I  K  T  I  V  T  R   20

 61 ATCAGTGACATTTCACACATGCAGTCTGTCTCCTCCAAACAGAGGGTCACCGGTTTGGAC  120
 21   I  S  D  I  S  H  M  Q  S  V  S  S  K  Q  R  V  T  G  L  D   40

121 TTCATCCCTGGGCTCCATCCTGTCCTGAGTTTGTCCAAGATGGACCAGACCCTGGCGATC  180
 41   F  I  P  G  L  H  P  V  L  S  L  S  K  M  D  Q  T  L  A  I   60

181 TACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATCCAAATATCGAATGACCTG  240
 61   Y  Q  Q  I  L  T  S  L  P  S  R  N  V  I  Q  I  S  N  D  L   80

241 GAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCCTCCAAGAGCTGCCCCTTGCCCAGC  300
 81   E  N  L  R  D  L  L  H  L  L  A  S  S  K  S  C  P  L  P  S  100

301 AGGGCCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCCTGGAAGCCTCCCTCTACTCCACG  360
101   R  A  L  E  T  L  E  S  L  G  G  V  L  E  A  S  L  Y  S  T  120

361 GAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGACATGCTGCGGCACGTGGAC  420
121   E  V  V  A  L  S  R  L  Q  G  A  L  Q  D  M  L  R  H  V  D  140

421 CTCAGCCCTGGCTGC                                               435
141   L  S  P  G  C                                               145
```

FIG. 4


10 20 30 40 50
PIG 1 ATGCGCTGTG GACCCCTGTG CCGATTCCTG CTGGCTTTGG GC-TATCTGT 50
HUMAN 1 ATGCATTGGG GAACCCTGTG CGGATTCTTG -TGGCTTTGG GCCTATCTTT 50
MOUSE 1 ATGTGCTGGA GACCCCTGTG TCGGTTCCTG -TGGCTTTGG TCCTATCTGT 50
60 70 80 90 100
PIG 51 CCTACGTTGA AGCCGTGCCC ATCTGGAGAG TCCAGGATGA CACCAAAACC 100
HUMAN 51 TCTATGTCCA AGCTGTGCCC ATCCAAAAAG TCCAAGATGA CACCAAAACC 100
MOUSE 51 CTTATGTTCA AGCAGTGCCT ATCCAGAAAG TCCAGGATGA CACCAAAACC 100
110 120 130 140 150
PIG 101 CTCATCAAGA CGATTGTCAC CAGGATCAGT GACATTTCAC ACATGCAGTC 150
HUMAN 101 CTCATCAAGA CAATTGTCAC CAGGATCAAT GACATTTCAC ACACGCAGTC 150
MOUSE 101 CTCATCAAGA CCATTGTCAC CAGGATCAAT GACATTTCAC ACACGCAGTC 150
160 170 180 190 200
PIG 151 TGTCTCCTCC AAACAGAGGG TCACCGGTTT GGACTTCATC CCTGGGCTCC 200
HUMAN 151 AGTCTCCTCC AAACAGAAAG TCACCGGTTT GGACTTCATT CCTGGGCTCC 200
MOUSE 151 GGTATCCGCC AAGCAGAGGG TCACTGGCTT GGACTTCATT CCTGGGCTTC 200
210 220 230 240 250
PIG 201 ATCCTGTCCT GAGTTTGTCC AAGATGGACC AGACCCTGGC GATCTACCAA 250
HUMAN 201 ACCCCATCCT GACCTTATCC AAGATGGACC AGACACTGGC AGTCTACCAA 250
MOUSE 201 ACCCCATTCT GAGTTTGTCC AAGATGGACC AGACTCTGGC AGTCTATCAA 250
260 270 280 290 300
PIG 251 CAGATCCTCA CCAGTCTGCC TTCCAGAAAT GTGATCCAAA TATCGAATGA 300
HUMAN 251 CAGATCCTCA CCAGTATGCC TTCCAGAAAC GTGATCCAAA TATCCAACGA 300
MOUSE 251 CAGGTCCTCA CCAGCCTGCC TTCCCAAAAT GTGCTGCAGA TAGCCAATGA 300
310 320 330 340 350
PIG 301 CCTGGAGAAC CTCCGGGACC TTCTCCACCT GCTGGCCTCC TCCAAGAGCT 350
HUMAN 301 CCTGGAGAAC CTCCGGGATC TTCTTCACGT GCTGGCCTTC TCTAAGAGCT 350
MOUSE 301 CCTGGAGAAT CTCCGAGACC TCCTCCATCT GCTGGCCTTC TCCAAGAGCT 350
360 370 380 390 400
PIG 351 GCCCCTTGCC CAG---CAGG GCCCTGGAGA CCTTGGAGAG CCTGGGCGGC 400
HUMAN 351 GCCACTTGCC CTGGGCCAGT GGCCTGGAGA CCTTGGACAG CCTGGGGGCT 400
MOUSE 351 GCTCCCTGCC TCAGACCAGT GGCCTGCAGA AGCCAGAGAG CCTGGATGGC 400
410 420 430 440 450
PIG 401 GTCCTGGAAG CCTCCCTCTA CTCCACGGAG GTGGTGGCCC TGAGCAGGCT 450
HUMAN 401 GTCCTGGAAG CTTCAGGCTA CTCCACAGAG GTGGTGGCCC TGAGCAGGCT 450
MOUSE 401 GTCCTGGAAG CCTCACTCTA CTCCACAGAG GTGGTGGCTT TGAGCAGGCT 450
460 470 480 490 500
PIG 451 GCAGGGGGCT CTGCAGGACA TGCTGCGGCA GCTGGACCTC AGCCCTGGCT 500
HUMAN 451 GCAGGGGTCT CTGCAGGACA TGCTGTGGCA GCTGGACCTC AGCCCTGGGT 500
MOUSE 451 GCAGGGCTCT CTGCAGGACA TTCTTCAACA GTTGGATGTT AGCCCTGAAT 500
510 520 530 540 550
PIG 501 GCTGA..... 550
HUMAN 501 GCTGA..... 550
MOUSE 501 GCTGA..... 550

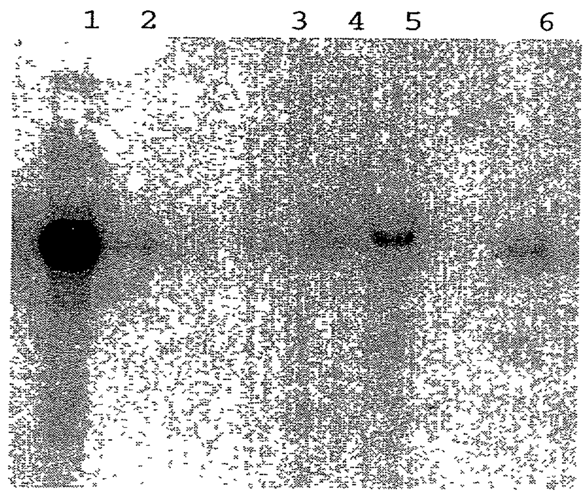


FIG. 5

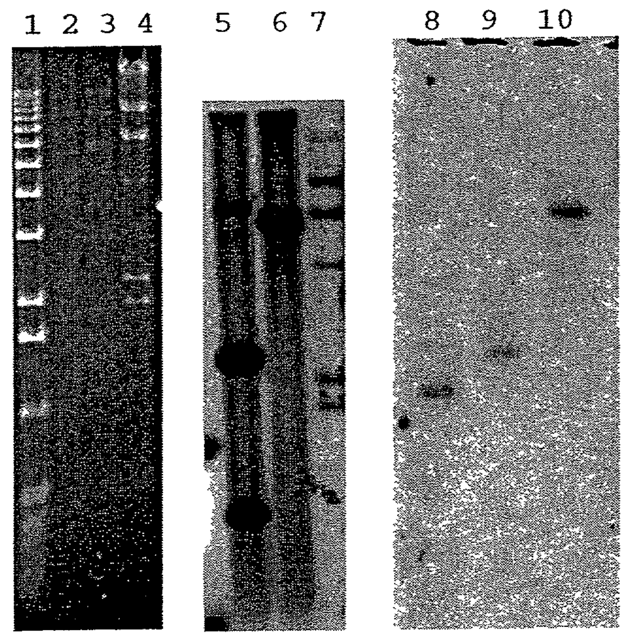


FIG. 6

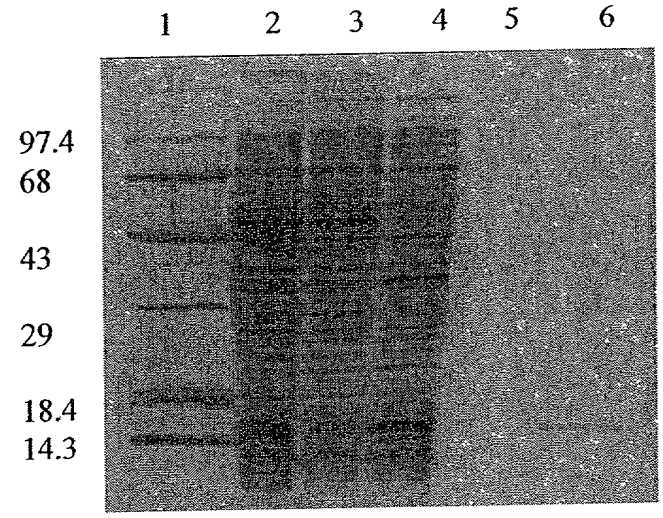


FIG. 7

FIG. 8

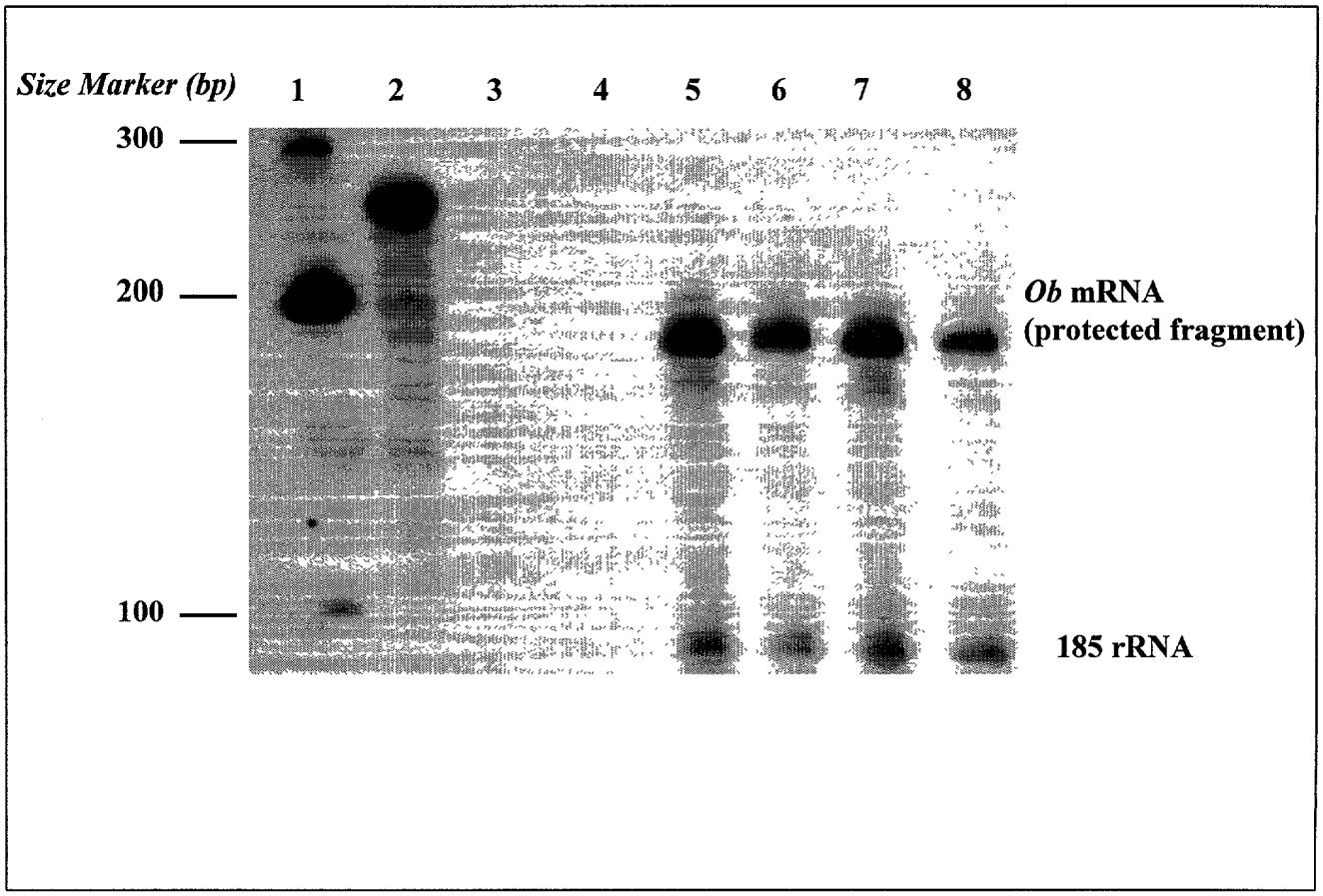

Size Marker (bp)
1
2
3
4
5
6
7
8
300
200
100
Ob mRNA
(protected fragment)
185 rRNA

FIG. 9

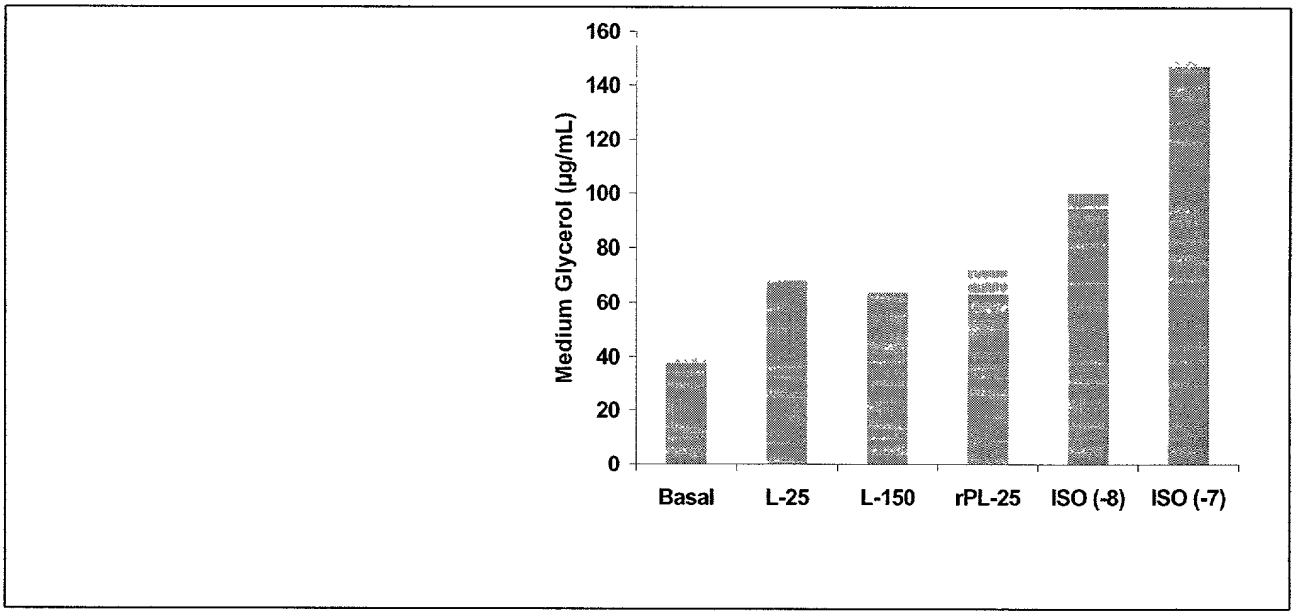

Medium Glycerol (µg/mL)
160
140
120
100
80
60
40
20
0
Basal
L-25
L-150
rPL-25
ISO (-8)
ISO (-7)

FIG. 10

Western blot of recombinant human and porcine leptin with the polyclonal antibody to synthetic peptide based on the C-terminal sequence of porcine leptin.

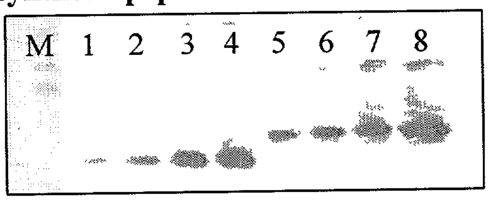


FIG. 11

A polyclonal antibody to recombinant porcine leptin immunoprecipaitates leptin from pig serum, cerebral spinal fluid (CSF), and adipose extracts.